

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/862,442DATE: 07/30/97  
TIME: 10:42:39

INPUT SET: S19288.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

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## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Shyjan, Andrew W.

(ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
DIAGNOSIS, PREVENTION AND TREATMENT OF TUMOR  
PROGRESSION

(iii) NUMBER OF SEQUENCES: 9

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fish & Richardson P.C.  
(B) STREET: 225 Franklin Street  
(C) CITY: Boston  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02110-2804

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 23-MAY-1997  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/623,679  
(B) FILING DATE: 29-MAR-1996

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/412,431  
(B) FILING DATE: 29-MAR-1995

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Fasse, J. Peter  
(B) REGISTRATION NUMBER: 32,983  
(C) REFERENCE/DOCKET NUMBER: 07334/004002

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617/542-5070

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47 (B) TELEFAX: 617/542-8906  
48 (C) TELEX: 200154  
49

50 (2) INFORMATION FOR SEQ ID NO:1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 186 base pairs  
53 (B) TYPE: nucleic acid  
54 (C) STRANDEDNESS: single  
55 (D) TOPOLOGY: linear  
56  
57

58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

59  
60 GGTGCTGGAG TACCTCATGG GCGGTGCCTA CCGCTGCAAC TACACTCGGA AAAGCTTCCG 60  
61  
62 GACTCTCTAC AACAACTTGT TTGGCCCTAA GAGGGTAGAG CTCAGCAGAC ACACAGTGTC 120  
63  
64 CTGTGCCTCC CAGAGTAACA TGTGGTTCCT TGATGTGCTT CCCCAAAGC CCACCTGTGC 180  
65  
66 AGAATG 186  
67

68 (2) INFORMATION FOR SEQ ID NO:2:

69 (i) SEQUENCE CHARACTERISTICS:

70 (A) LENGTH: 2729 base pairs  
71 (B) TYPE: nucleic acid  
72 (C) STRANDEDNESS: single  
73 (D) TOPOLOGY: linear  
74  
75

76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

77  
78 AAGGAGGCTA GGCTGCACCC TTCCCCTTG CTCAGCAGCT GAGGCAGGGT CAGAAAGCAT 60  
79  
80 GGATAGAGAA GACATTTTGC AAAAGGGAAT GCATCTTTGT AATTCCCAGT ACAAAGACC 120  
81  
82 CTAACAGATG TTGCTGTGGT CAGCTCACTA ACCAGCACAT CCCCCTTTG CCGAGTGGGG 180  
83  
84 CTCCCAGCAC AACAGGAGAG GACACCAAGC AGGCAGACAC GCAGTCCGGG AAATGGTCTG 240  
85  
86 TCAGCAAACA CACCCAGAGC TACCCAACAG ACTCCTATGG GATTCTTGAA TTCCAGGGTG 300  
87  
88 GGGGTTACTC CAATAAAGCC ATG TAC ATC CGA GTC TCC TAC GAC ACC AAG 350  
89 Met Tyr Ile Arg Val Ser Tyr Asp Thr Lys  
90 1 5 10  
91  
92 CCA GAT TCC CTG CTC CAC CTC ATG GTG AAG GAC TGG CAG CTG GAG CTC 398  
93 Pro Asp Ser Leu Leu His Leu Met Val Lys Asp Trp Gln Leu Glu Leu  
94 15 20 25  
95  
96 CCG AAG CTC TTG ATA TCT GTG CAC GGA GGC CTC CAA AGC TTC GAG ATG 446  
97 Pro Lys Leu Leu Ile Ser Val His Gly Gly Leu Gln Ser Phe Glu Met  
98 30 35 40  
99

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100	CAG TCC AAA CTG AAG CAG GTG TTT GGG AAA GGT CTG ATC AAG GCT GCC	494
101	Gln Ser Lys Leu Lys Gln Val Phe Gly Lys Gly Leu Ile Lys Ala Ala	
102	45 50 55	
103		
104	ATG ACC ACG GGG GCG TGG ATC TTC ACC GGG GGT GTG AGC ACT GGT GTC	542
105	Met Thr Thr Gly Ala Trp Ile Phe Thr Gly Gly Val Ser Thr Gly Val	
106	60 65 70	
107		
108	GTC AGC CAT GTG GGG GAT GCC TTG AAA GAC CAC TCC TCC AAG TCC AGA	590
109	Val Ser His Val Gly Asp Ala Leu Lys Asp His Ser Ser Lys Ser Arg	
110	75 80 85 90	
111		
112	GGC CGG CTC TGT GCT ATA GGA ATT GCT CCC TGG GGC ATG GTG GAG AAC	638
113	Gly Arg Leu Cys Ala Ile Gly Ile Ala Pro Trp Gly Met Val Glu Asn	
114	95 100 105	
115		
116	AAG GAA GAC CTG ATT GGA AAA GAT GTA ACA AGA GTC TAT CAG ACC ATG	686
117	Lys Glu Asp Leu Ile Gly Lys Asp Val Thr Arg Val Tyr Gln Thr Met	
118	110 115 120	
119		
120	TCC AAC CCT CTG AGC AAG CTC TCT GTG CTC AAC AAT TCC CAC ACT CAC	734
121	Ser Asn Pro Leu Ser Lys Leu Ser Val Leu Asn Asn Ser His Thr His	
122	125 130 135	
123		
124	TTC ATC TTG GCT GAC AAC GGC ACC CTG GGC AAG TAT GGT GCT GAG GTG	782
125	Phe Ile Leu Ala Asp Asn Gly Thr Leu Gly Lys Tyr Gly Ala Glu Val	
126	140 145 150	
127		
128	AAG CTT CGA AGA CAG CTG GAA AAA CAC ATC TCC CTG CAG AAG ATC AAC	830
129	Lys Leu Arg Arg Gln Leu Glu Lys His Ile Ser Leu Gln Lys Ile Asn	
130	155 160 165 170	
131		
132	ACA AGG CTG GGC CAG GGT GTA CCT GTC GTG GGC CTA GTG GTA GAA GGT	878
133	Thr Arg Leu Gly Gln Gly Val Pro Val Val Gly Leu Val Val Glu Gly	
134	175 180 185	
135		
136	GGT CCT AAC GTG GTT TCT ATC GTC CTG GAG TAT CTC AAA GAA GAC CCT	926
137	Gly Pro Asn Val Val Ser Ile Val Leu Glu Tyr Leu Lys Glu Asp Pro	
138	190 195 200	
139		
140	CCT GTC CCT GTG GTG GTT TGC GAT GGC AGT GGA CGT GCC TCT GAC ATT	974
141	Pro Val Pro Val Val Val Cys Asp Gly Ser Gly Arg Ala Ser Asp Ile	
142	205 210 215	
143		
144	TTG TCC TTC GCA CAC AAA TAC TGC GAC GAA GGA GGA GTC ATA AAC GAG	1022
145	Leu Ser Phe Ala His Lys Tyr Cys Asp Glu Gly Gly Val Ile Asn Glu	
146	220 225 230	
147		
148	TCC CTG CGG GAC CAG CTT CTA GTT ACC ATT CAG AAA ACA TTT AAT TAC	1070
149	Ser Leu Arg Asp Gln Leu Leu Val Thr Ile Gln Lys Thr Phe Asn Tyr	
150	235 240 245 250	
151		
152	AGC AAG TCC CAG TCG TAT CAG CTG TTT GCA ATT ATC ATG GAG TGC ATG	1118

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153	Ser	Lys	Ser	Gln	Ser	Tyr	Gln	Leu	Phe	Ala	Ile	Ile	Met	Glu	Cys	Met	
154					255					260					265		
155																	
156	AAG	AAG	AAA	GAA	CTC	GTC	ACT	GTG	TTT	CGG	ATG	GGT	TCC	GAG	GGT	CAG	1166
157	Lys	Lys	Lys	Glu	Leu	Val	Thr	Val	Phe	Arg	Met	Gly	Ser	Glu	Gly	Gln	
158				270					275					280			
159																	
160	CAA	GAT	GTC	GAG	ATG	GCA	ATT	TTA	ACT	GCC	TTG	CTC	AAA	GGA	ACC	AAC	1214
161	Gln	Asp	Val	Glu	Met	Ala	Ile	Leu	Thr	Ala	Leu	Leu	Lys	Gly	Thr	Asn	
162			285					290					295				
163																	
164	GCA	TCA	GCT	CCA	GAT	CAG	CTG	AGC	TTG	GCC	CTG	GCT	TGG	AAC	CGG	GTC	1262
165	Ala	Ser	Ala	Pro	Asp	Gln	Leu	Ser	Leu	Ala	Leu	Ala	Trp	Asn	Arg	Val	
166		300					305					310					
167																	
168	GAC	ATA	GCG	CGA	AGC	CAG	ATC	TTC	GTC	TTT	GGC	CCA	CAC	TGG	CCG	CCA	1310
169	Asp	Ile	Ala	Arg	Ser	Gln	Ile	Phe	Val	Phe	Gly	Pro	His	Trp	Pro	Pro	
170	315					320					325					330	
171																	
172	CTG	GGA	AGC	CTG	GCC	CCT	CCT	GTG	GAC	ACC	AAA	GCC	GCA	GAG	AAG	GAA	1358
173	Leu	Gly	Ser	Leu	Ala	Pro	Pro	Val	Asp	Thr	Lys	Ala	Ala	Glu	Lys	Glu	
174				335					340					345			
175																	
176	AAG	AAG	CCA	CCC	ACA	GCC	ACC	ACC	AAG	GGG	AGA	GGA	AAA	GGA	AAA	GGC	1406
177	Lys	Lys	Pro	Pro	Thr	Ala	Thr	Thr	Lys	Gly	Arg	Gly	Lys	Gly	Lys	Gly	
178			350						355					360			
179																	
180	AAG	AAG	AAA	GGC	AAA	GTG	AAA	GAG	GAA	GTG	GAG	GAA	GAG	ACG	GAC	CCC	1454
181	Lys	Lys	Lys	Gly	Lys	Val	Lys	Glu	Glu	Val	Glu	Glu	Glu	Thr	Asp	Pro	
182			365					370					375				
183																	
184	CGG	AAG	CTT	GAG	CTG	CTC	AAC	TGG	GTG	AAT	GCC	CTG	GAG	CAA	GCC	ATG	1502
185	Arg	Lys	Leu	Glu	Leu	Leu	Asn	Trp	Val	Asn	Ala	Leu	Glu	Gln	Ala	Met	
186		380					385					390					
187																	
188	CTG	GAT	GCT	CTT	GTC	CTA	GAT	CGG	GTG	GAC	TTT	GTA	AAG	CTC	CTG	ATT	1550
189	Leu	Asp	Ala	Leu	Val	Leu	Asp	Arg	Val	Asp	Phe	Val	Lys	Leu	Leu	Ile	
190	395					400					405					410	
191																	
192	GAA	AAC	GGA	GTG	AAC	ATG	CAG	CAT	TTC	CTC	ACC	ATC	CCG	AGG	CTG	GAG	1598
193	Glu	Asn	Gly	Val	Asn	Met	Gln	His	Phe	Leu	Thr	Ile	Pro	Arg	Leu	Glu	
194				415						420				425			
195																	
196	GAG	CTA	TAC	AAC	ACC	AGA	CTG	GGC	CCA	CCA	AAC	ACC	CTT	CAT	CTG	CTG	1646
197	Glu	Leu	Tyr	Asn	Thr	Arg	Leu	Gly	Pro	Pro	Asn	Thr	Leu	His	Leu	Leu	
198			430					435					440				
199																	
200	GTG	CGG	GAT	GTA	AAG	AAG	AGC	AAC	CTT	CCA	CCT	GAT	TAC	CAC	ATC	AGC	1694
201	Val	Arg	Asp	Val	Lys	Lys	Ser	Asn	Leu	Pro	Pro	Asp	Tyr	His	Ile	Ser	
202			445					450					455				
203																	
204	CTC	ATT	GAT	ATA	GGA	CTG	GTG	CTG	GAG	TAC	CTC	ATG	GGC	GGT	GCC	TAC	1742
205	Leu	Ile	Asp	Ile	Gly	Leu	Val	Leu	Glu	Tyr	Leu	Met	Gly	Gly	Ala	Tyr	

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	460	465	470	
206				
207				
208	CGC TGC AAC TAC ACT CGG AAA AGC TTC CGG ACT CTC TAC AAC AAC TTG			1790
209	Arg Cys Asn Tyr Thr Arg Lys Ser Phe Arg Thr Leu Tyr Asn Asn Leu			
210	475	480	485	490
211				
212	TTT GGC CCT AAG AGG GTA GAG CTC AGC AGA CAC ACA GTG TCC TGT GCC			1838
213	Phe Gly Pro Lys Arg Val Glu Leu Ser Arg His Thr Val Ser Cys Ala			
214		495	500	505
215				
216	TCC CAG AGT AAC ATG TGG TTC CTT GAT GTG CTT CCC CAA AAG CCC ACC			1886
217	Ser Gln Ser Asn Met Trp Phe Leu Asp Val Leu Pro Gln Lys Pro Thr			
218		510	515	520
219				
220	TGT GCA GAA TGC AAC TCT TCA CCT CAC CTG TCC CAA ACT GAC ATC ACC			1934
221	Cys Ala Glu Cys Asn Ser Ser Pro His Leu Ser Gln Thr Asp Ile Thr			
222		525	530	535
223				
224	CCA CCT CTG CCC T GACACCCAGT GCAGGGCCCTC CTAGCTTTCA CATGCAGCCA			1987
225	Pro Pro Leu Pro			
226	540			
227				
228	TTCACATCGC CTCTCAAGAC TGGGCCAGGC AGTGCAACCT GTCAAGCATG TCTGTCCCTCC			2047
229				
230	CCTCCTTCCT ACAATAGCCC CCCCTCTGGG CCCCATGCCT CTGCTCTCTC AGCCCGTTCT			2107
231				
232	CCTCCCCACT GATCACTGGC GCTCCTGTTG TCTTCCAAGG CAAGGAACAA GGAAAAGCAT			2167
233				
234	CTTTTTGCCC ACAAAGTTT AGGGCTCCCC GCTGTTCAAC CATAGCCAAC CTCACTGTAC			2227
235				
236	ATCGGAGTCA TCCAGGCCAG CTGCCACACA CAAGCCTTCC CCACCCTATC CCAATAGACC			2287
237				
238	CTATTCCTCC ATCAAAATCA AAGCTAACTC CTGGCCTGCC ACATTGCTTC TTCTTGCTCC			2347
239				
240	AGCCTGTTAA ACCTCCAATA AATGTCAGAT CTGTGGGAAG CCTTCCTCAC TCTCACTCCA			2407
241				
242	CAGTTTGTAC AGAGAGCGAG AGCCTCGTTT GGTTCCTACTT ACAAGGAAGG CTTTGTGTCT			2467
243				
244	GTCTGTCCCTT CCCAACTGAC TTCTGTTGAC AGAAGCAGTT TCCACATGAA AGCGTTGACT			2527
245				
246	CACCTGGATG TTGTCATTAA TTAATAGTGA TACAAAATAT TGACACTTCT TTTCCCTGCTT			2587
247				
248	CTTTGTTATG CAGCCGAAAG CACTTAAGCT TCTGGGAATG GAAGTAAGTA GGACATGTTT			2647
249				
250	GTGGCAGTTT ATTTACTATA TATACCTTTG TCATTCTGTG GAAGCAAAAA TTGCAATGTT			2707
251				
252	TTCCATGAAT AAAGCTCGTG CC			2729
253				
254				
255				
256	(2) INFORMATION FOR SEQ ID NO:3:			
257				
258	(i) SEQUENCE CHARACTERISTICS:			

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**SEQUENCE VERIFICATION REPORT**  
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